MicroRNA expression profiles on hepatocellular carcinoma cells with different intracellular hepatitis C viral load

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Objectives: The HCV infection and replication varies among individual hepatocytes in chronic HCV infection by identifying hepatocytes with different HCV viral RNA. We have previously established a Fluorescence-activated cell sorting (FACS) protocol to study the effects of different intracellular viral loads in HCV-infected cell populations. In the present study we aimed to further study the microRNA (miR) expression more detail on different viral load cells.

Methods: We used JFH1-EYFP viral florescence intensity to sort the high and low viral load cells after 5 days infection in vitro which has been shown in our previous study that infected cells efficiently and accurately discriminated between high- and low-viral load cell populations. The next generation sequence-RNA sequence was used to clarify the mRNA and miRNA gene network between HCV-high and HCV-low infected cells.

Results: The mRNA and miRNA expression profiles in different viral load cell populations were analyzed by using the NGS dataset and miRNA microarray dataset. We found that miR-194, miR-215 and miR-10b were preferentially highly expressed in low viral load cells, which was further validated (Fig 1). We found that high viral loads were associated cell inflammation- and cell death-associated pathway (Fig 2); low viral loads were associated many stress response- and cell adhesion molecular (CAMs)-related genes (Fig 3).

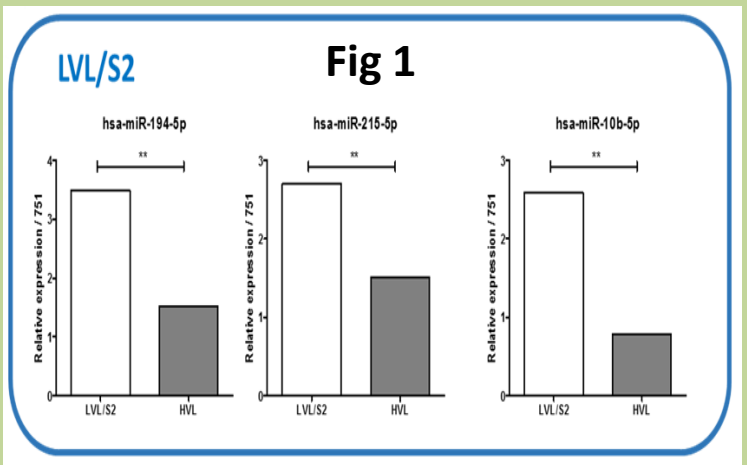

Fig 1

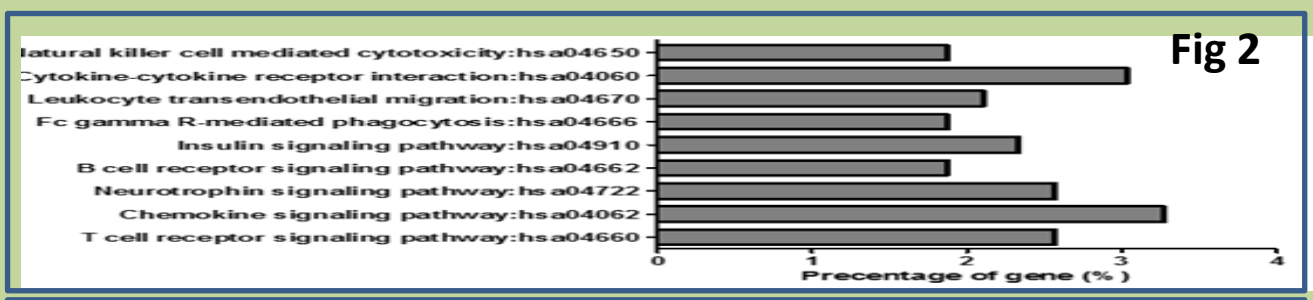

Fig 2

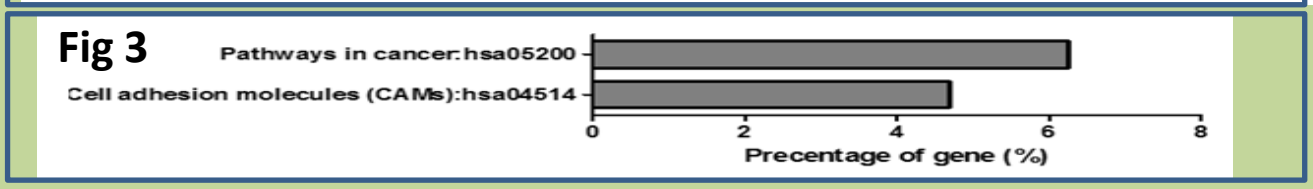

Fig 3

Conclusions: We have established a cell sorting protocol to study the effects of viral loads in HCV-infected cell populations which demonstrated different gene network between HCV-high and HCV-low infected cells in JFH1-EYFP infectious cells. Our results may provide board gene regulation map between high and low viral load cell populations.